

In the Claims:

1-18. (canceled).

19. (currently amended). A method of transforming trees to modify fibre characteristics in trees, the method comprising stably incorporating into the plant genome a chimaeric gene comprising a promoter and a nucleic acid sequence encoding an expansin capable of modifying at least one of: fibre cell wall extension, tree height or internode length, or a combination thereof; said nucleic acid sequence selected from the group consisting of [of] SEQ ID NOS: 1-6, the cucumber expansin sequence cucumber Ex29 (GenBank Accession No. U30382) SEQ ID NO: 9, parts thereof, sequences substantially similar thereto and having the same function, and combinations thereof; and regenerating a tree having an altered genome.

20. (previously presented). A method according to Claim 19, wherein said nucleic acid sequence is derived from *Eucalyptus* or cucumber.

21. (previously presented). A method according to Claim 19, wherein said nucleic acid sequence is an mRNA, a cDNA sequence or a genomic DNA.

22. (previously presented). A method according to Claim 19, wherein said nucleic acid sequence, or part thereof, is arranged in a normal reading frame direction or in a reverse reading frame direction.

23. (previously presented). A method according to Claim 22, wherein said nucleic acid, or part thereof, is arranged in the normal reading frame direction and a decrease in internode length and/or plant height is achieved.

24. (previously presented). A nucleic acid sequence encoding a gene capable of modifying at least one of: fibre cell wall extension, tree height or internode length, or a combination thereof;

wherein the nucleic acid sequence is selected from the group consisting of SEQ ID NOs: 1-6, parts thereof, sequences substantially similar thereto and having the same function, and combinations thereof.

25. (previously presented). A chimaeric gene comprising a nucleic acid sequence according to claim 24 and a promoter.

26. (previously presented). A chimaeric gene according to Claim 25, wherein said chimaeric gene further comprises a terminator.

27. (previously presented). A chimaeric gene according to Claim 25, wherein said chimaeric gene comprises said nucleic acid sequence as said nucleic acid sequence exists in nature, with or without introns, complete with endogenous promoter, terminator, and other regulatory sequences.

28. (previously presented). A chimaeric gene according to Claim 25, wherein said chimaeric gene comprises said nucleic acid sequence, with or without introns, combined with a heterologous promoter, terminator and/or other regulatory sequences.

29. (previously presented). A chimaeric gene according to Claim 25, wherein said promoter is selected from the group consisting of the cauliflower mosaic virus 35S promoter (CaMV35S), the cauliflower mosaic virus 19S promoter (CaMV19S), the nopaline synthase promoter, the *rolC*, patatin or *petE* promoters, the AlcR/AlcS promoter and a fibre-related promoter.

30. (previously presented). A chimaeric gene according to Claim 25, wherein said nucleic acid sequence, or part thereof, is arranged in a normal reading frame direction or in a reverse reading frame direction.

31. (previously presented). A method according to Claim 19, wherein said chimaeric gene is a chimaeric gene as claimed in Claims 25-30.

32. (previously presented). A tree comprising a chimaeric gene of Claims 25-30.
33. (previously presented). A plant cell comprising a chimaeric gene of Claims 25-30.
34. (previously presented). A tree transformed according to the method of Claims 19-23 or 31.
35. (previously presented). A tree as claimed in Claim 34, said tree being a eucalypt, aspen, pine or larch.
36. (previously presented). A seed of a tree transformed according to the method of Claims 19-23 or 31.